

SEQUENCE LISTING

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<120> METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS
USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC
PROTEIN

<130> 690068.405C3

<140> US 10/015,540

<141> 2001-12-11

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 513

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(513)

<400> 1

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Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu Ala
1 5 10 15

ctc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 75
Thr Ala Ser Thr Ser Asp His Ala Arg His His Ile Ile Ile Ala His

tta gtc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 105
Asp Asp Thr Gly Ile Leu Asp Ser Ile His Arg Ile Ile His Gly Asp
35 40 45

tta ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 135
Asp His Ala Ile Tyr Arg His Ser His Lys Asp Ser His His Ile Ala
65 70 75

	85	90	95	
cgc aca cca ccc ccc tog cag gga aag ggg aga gga ctg ttc ctg agc				336
Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser				
	100	105	110	
aga ttt agc tgg ggg ggc gaa ggt cag aga cca gga ttt gtc tac gga				344
Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr Gly				
	115	120	125	
ggc aga ggc tcc gac tat aaa tog gct cac aag gga ttc aag gga gtc				432
Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly Val				
	130	135	140	
gat gcc cag gcc aag ctt tcc aaa att ttt aag ctg gga gaa aga gat				480
Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg Asp				
	145	150	155	160
agt cgc tct gga tca ccc atg gct aga cgc tga				513
Ser Arg Ser Gly Ser Pro Met Ala Arg Arg *				
	165	170		

<210> 2

<211> 170

<212> PRT

<213> Homo sapiens

<400> 2

Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu Ala				
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Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg His				
20	25	30		
Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly Asp				
35	40	45		
Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro Ala				
50	55	60		
Arg Thr Ala His Tyr Gly Ser Ile Ile Ala Lys Ser His Gly Arg Thr				
65	70	75		
Arg Asp Thr Asp Ile Val Thr His His His Tyr Asp Ile Thr Thr Ile				
80	85	90		
Arg Thr Ile Ile Ile Ser His Gly Lys Gly Arg Gly Leu Ser Leu Ser				
100	105	110		
Arg Phe Ser Trp Gly Ala Gln Gly Gln Arg Ile Gly Ile Gly Tyr Gly				
115	120	125		
Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Tyr Gly Ile Tyr Gly Val				
130	135	140		

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<400> 3
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 <211> 516
 <212> DNA
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<220>
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 <222> (1)...(516)

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 Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu
 1 5 10 15

gcc aca gca agt acc atg gac cat gcc agg cat gcc ttc ctg cca agg 96
 Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg
 20 25 30

cac aga gac acg gcc atc ctt gac tcc atc ggg cgc ttc ttt gcc ggt 144
 His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly
 35 40 45

gac agg ggt gcg cca aag cgg gcc tct gcc aag gac tca cac cac ccc 192
 Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro
 50 55 60

aca aga act gct cac tat gcc tcc ctg ccc cag aac tca cac gcc ctg 240
 Ala Ala Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg
 65 70 75

ctt tat att tta att ccc att tta att tta tta att att att att att 288
 Thr His Arg Ala Asn Pro Val Val His Ile Phe Lys Asn Leu Val Thr
 80 85 90 95

att gcc aca cca ccc arg tcc cag gga cag gtt aca gga ctg ttt ctg 336
 Pro Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Ala Gly Leu Ser Leu
 100 105 110 115

gac gat gag gaa gga aac att tcc aaa att att aac att gta gta aca 45
 Val Asp Ala Ser Gly Thr Leu Ser Lys Ile Ile Lys Leu Gly Gly Arg
 145 150 155 160

gat agt ggt tct gga tca ccc atg ggt aga ggc tga 115
 Asp Ser Arg Ser Gly Ser Pro Met Ala Arg Arg *
 165 170

<210> 5

<211> 171

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu
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 Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg
 20 25 30
 His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly
 35 40 45
 Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro
 50 55 60
 Ala Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg
 65 70 75 80
 Thr Gln Asp Gln Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr
 85 90 95
 Pro Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu
 100 105 110
 Ser Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr
 115 120 125
 Gly Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly
 130 135 140
 Val Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg
 145 150 155 160
 Arg Ser Arg Ser Gly Ser Leu Met Ala Arg Arg
 165 170